

Sequence logo showing the conservation of amino acids across a set of 34854114.m homologs. The x-axis represents positions 410 to 600. The y-axis lists 34 homologs. Each position has four bars representing A, T, C, and G. The height of each bar indicates the probability of that nucleotide at that position.

	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	10
34854114.m	HCGAYSPGSPSEHLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFIVRCEEP	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854080.m	HCSAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEKETSPGABQNLTPPEMS	PRESEDDKKQQQAPRDPDV	NAMEYICFOVETKDSBON	IQMASYFELQ	EEIRQDSTK											
34864947.m	CGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEKETSPGABQNLTPPEMS	PRESEDDKKQQQAPRDPDV	NAMEYICFOVETKDSBON	IQMASYFELQ	EEIRQDSTK											
34854082.m	CGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SMIEQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34864924.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34864955.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFIVRCEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34853866.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFIVRCEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854096.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34864941.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854112.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854108.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34864935.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34853834.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854122.m	HCGAYSPGSPERLGLLYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSEELNLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854118.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELDLSSKLRLVPNPF	RACKAMKHP	FKEHWNCLGPYEEM	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854104.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELDLSSKLRLVPNPF	RACKAMKHP	FKEHWNCLGPYEEM	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854106.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELDLSSKLRLVPNPF	RACKAMKHP	FKEHWNCLGPYEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34882390.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854084.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854120.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34853870.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854098.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854092.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854078.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854116.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34853848.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34853854.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
27715933.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854124.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854100.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854076.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34853862.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34854088.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
34883072.m	HCGTYSPGSPELLGLHYD	GKNDMIGVVLYPMVVKLPPFD	SVIQELQKVVAQVYPAPCR	VSELELLSLLSQQLVNPMLYR	TASEVMKHA	FKEHKGCFGRYEEEL	DPLRPDPDEILPAMKCMFQASV	VIKYSLHKRYNEEMATY	CFLQQQALGYC	CTAQAAQVSPIAAPP	SLDP									
1ia8_A	MCCGIPSPSEHLKRRFFH	AEPVDWMCVGIVLPAEDGEPPWD	PDSCEBYSDWKEKKYIYLNPWKK	IDSADPLALLHKILVPNSARTID	DICK															
2phk_A	VCGGIPSPSEHLKRRFFH	AEPVDWMCVGIVLPAEDGEPPWD	PDSCEBYSDWKEKKYIYLNPWKK	IDSADPLALLHKILVPNSARTID	DICK															
1kwp_A	PCVTPYVVAPEVLGPKPEK	YDKSCDMVLSHVIMYILLCCYI	PFYNSNHGLAISPCMKRIMCQEY	EFPPNEWSEV	SEEVWMLRNLLKPEPTOR	TFEPNPHIMOSTKVPQTPLHTS														
1jkk_A	IFGIPSEPVAVIENYEP	LGEEADWVLEVIVIPLL	GASPLFLGDTIQETLAN	VAVNIEFEDEYFSNI	ALAND	TFRRELVEDPKR	IQDSDPCHP	PRK												

	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	12
34854114.m	AAAFLRLRKR																			
34854080.m	AAAFLRLRKR																			
34864947.m	AAAFLRLRKR																			
34854082.m	AAAFLRLRKR																			
34864924.m	AAAFLRLRKR																			
34864955.m	AAAFLRLRKR																			
34853866.m	AAAFLRLRKR																			
34854096.m	AAAFLRLRKR																			
34864941.m	AAAFLRLRKR																			
34854112.m	AAAFLRLRKR																			
34854084.m	AAAFLRLRKR																			
34854122.m	AAAFLRLRKR																			
34854108.m	AAAFLRLRKR																			
34864935.m	AAAFLRLRKR																			
34853834.m	AAAFLRLRKR																			
34854120.m	AAAFLRLRKR																			
34853870.m	AAAFLRLRKR																			
34854098.m	AAAFLRLRKR																			
34854092.m	AAAFLRLRKR																			
34864924.m	AAAFLRLRKR																			
34864955.m	AAAFLRLRKR																			
34853866.m	AAAFLRLRKR																			
34854096.m	AAAFLRLRKR																			
34864941.m	AAAFLRLRKR																			
34854112.m	AAAFLRLRKR																			
34854084.m	AAAFLRLRKR																			
34854122.m	AAAFLRLRKR																			
34854108.m	AAAFLRLRKR																			
34864935.m	AAAFLRLRKR																			
34853834.m	AAAFLRLRKR																			
34854120.m	AAAFLRLRKR																			
34853870.m	AAAFLRLRKR																			
34854098.m	AAAFLRLRKR																			
34854092.m	AAAFLRLRKR																			
34864924.m	AAAFLRLRKR																			
34864955.m	AAAFLRLRKR																			
34853866.m	AAAFLRLRKR																			
34854096.m	AAAFLRLRKR																			
34864941.m	AAAFLRLRKR																			
34854112.m	AAAFLRLRKR																			
34854082.m	AAAFLRLRKR																			
34864924.m	AAAFLRLRKR																			
34864955.m	AAAFLRLRKR																			
34853866.m	AAAFLRLRKR					</														

Sequence alignment showing protein fragments across multiple entries. The top section covers positions 1610 to 18, and the bottom section covers positions 1810 to 20. A color-coded legend indicates the amino acid type at each position.

Legend:

- Black: A, C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Red: F, L, V
- Blue: B, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Green: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Yellow: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Pink: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Cyan: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Magenta: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Orange: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Blue: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Green: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Yellow: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Magenta: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Cyan: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Orange: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Light Blue: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Light Green: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Light Yellow: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Light Magenta: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Light Cyan: C, D, E, G, H, I, K, M, N, P, S, T, W, Y
- Light Light Orange: C, D, E, G, H, I, K, M, N, P, S, T, W, Y

4410 4420 4430

.....|.....|.....|.....|.....|.....

34854114.m|.....|.....|.....|.....|.....
34854080.m|.....|.....|.....|.....|.....
34864947.m|.....|.....|.....|.....|.....
34854082.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34864924.m IANALIKLCCCC|RRKKP|RIGQNRIS|S|PEK|.....
34864955.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34853866.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854096.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34864941.m IANALIKLCCCC|RRKKP|RIGQNRIS|S|PEK|.....
34854112.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854108.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34864935.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34853834.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854122.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854118.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854104.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854106.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34882390.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854084.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854120.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34853870.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854098.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854092.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854078.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854116.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34853848.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34853854.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
27715933.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854124.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854100.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34854076.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34864953.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34853862.m IANALIKLCCCC|RRKKP|RIGQNRIS|PLIWPMLI|.....
34854088.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....
34883072.m IANALIKLCCCC|RRKKP|RIGQNRIS|PQK|.....

lia8_A
2phk_A
1kwp_A
1jkk_A